Farm specific risk factors for Campylobacter colonization of broilers in six European countries

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Local genes, for local bacteria: Geographical structuring in Campylobacter populations arising from local recombination

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Background: Geographical clustering is well documented in bacteria. The historical ancestry *Helicobacter pylori* can be reconstructed in concordance with human patterns of migration and *Mycobacterium tuberculosis* show enough allopatric clustering to successfully manage clinical outbreaks. In *Campylobacter*, source attribution from genomic data has been successful in distinguishing the host source of infection, but not geographical origin.

Objectives: We investigate biogeographical signals in genes that recombine rapidly to determine the extent of clustering in geographically distinct *Campylobacter* population genomes.

Methods: Whole genome sequences from 315 *Campylobacter* isolates from North America and the UK were analysed and the genetic inheritance of 15 closely matched pairs of isolates was quantified.

Results: Isolates from within the same country shared more DNA than isolates from different countries. Using a pairwise approach we identify regions of high diversity and test their correlation with geographical signal. The seven genes that demonstrated the greatest clustering by geography were used to attribute putative source using STRUCTURE. A further 383 UK clinical isolates were used to detect signals of foreign travel. Patient records indicated that 46 cases had travelled abroad less than two weeks prior to sampling and 34 (74%) of those *Campylobacter* genomes were deemed to be from a non-UK origin.

Conclusions: Detection of signals of biogeographical differences in *Campylobacter* genomes will contribute to improved source attribution of clinical Campylobacter infection and inform public policy and contribute to intervention strategies to reduce campylobacteriosis.

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This study was part of the EU financed project CamCon. The objective of the study was to identify on-farm risk factors for *Campylobacter* colonization of broiler flocks based on comparable data from six European countries. The data included explanatory variables from a large questionnaire concerning production, farm management procedures and conditions, climate data on mean temperature, sunshine hours, precipitation, as well as data on *Campylobacter* status of broiler flocks. Overall, the study comprised data from more than 6000 flocks. The data were analyzed using a generalized linear model using backwards elimination and forward selection. Due to the structure of the data, several models were explored, by applying different strategies for categorizing explanatory variables and for selection and elimination of variables in the model. The risk of broiler flocks becoming colonized with *Campylobacter* was clearly affected by country. In descending order; broiler flocks were more likely to be colonized in Poland, the UK, Spain, the Netherlands, Denmark and Norway due to country specific factors that could not be explained by the management and climate variables in the explored models. The seasonality in the prevalence of *Campylobacter* was described nicely by temperature, i.e. the number of positive flock increased with increasing temperatures. The age of broiler houses, presence of anterooms and barriers in all houses, designated tools for each house as well as length of downtime and the type of drinker systems were found to affect the risk of the broiler flocks becoming colonized by *Campylobacter*.
